

FIG. 1

SEQUENCE 1	: MOUSE HIDE1 (mHIDE1)
AMINO ACID LENGTH	: 222
MATCHING POSITION	: 1 - 222
SEQUENCE 2	: MOUSE SECRETORY HIDE1 (sHIDE1)
AMINO ACID LENGTH	: 192
MATCHING POSITION	: 1 - 192
SEQUENCE HOMOLGY	: 86.49 [%]
mHIDE1 : 1	MPWTILLFAS GSLAIPAPSI SLVPPYPSSH EDPIYISCTA PGDILGANFT LFRGGEVVQL *****
sHIDE1 : 1	MPWTILLFAS GSLAIPAPSI SLVPPYPSSH EDPIYISCTA PGDILGANFT LFRGGEVVQL *****
61	LQAPSDRDPV TFNVTGGGSG GGGEAAGGNF CCQYGVMEH SQQLSDFSQ QVQVSFPVPT *****
61	LQAPSDRDPV TFNVTGGGSG GGGEAAGGNF CCQYGVMEH SQQLSDFSQ QVQVSFP--- *****
121	WILALSLSLA GAVLFSGLVA ITVLVRKAKA KNLQKQRE SCWAQINFTN TDMSFDNSLF ***
118	-----AKA KNLQKQRE SCWAQINFTN TDMSFDNSLF *****
181	AISTKMTQED SVATLDGPR KRPTSASSSP EPPEFSTFRA CQ (SEQ ID NO:2) *****
151	AISTKMTQED SVATLDGPR KRPTSASSSP EPPEFSTFRA CQ (SEQ ID NO:4) *****

FIG. 2

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FIRST NUCLEOTIDE SEQUENCE
FILE NAME           : MOUSE  HIDE1  (mHIDE1)
NUCLEOTIDE LENGTH   : 666

SECOND NUCLEOTIDE SEQUENCE
FILE NAME           : HUMAN  HIDE1  (hHIDE1)
NUCLEOTIDE LENGTH   : 690
[73.932% / 702 bp]

mHIDE1:1' ATGCCCTGGACCATCTTGCTGTTGCATCTGGCTCCTTGGCCATCCCTGCACCATCCATC
*****
hHIDE1:1" ATGCCCTGGACCATCTTGCTCTTTGCAGCTGGCTCCTTGGCGATCCCAGCACCATCCATC

61' TCCTTGGTGCCCCCTACCCAAGCAGCCACGAGGACCCCATCTACATCTCGTGACAGCC
*****
61" CGGCTGGTGCCCCGTACCCAAGCAGCCAAGAGGACCCCATCCACATCGCATGCATGGCC

121' CCAGGGGACATCCTAGGGGCCAATTTTACCCTGTTCCGAGGGGGAGAGGTGGTCCAGCTA
** ** **
121" CCTGGGAACCTTCCCGGGGGCGAATTTTACACTGTATCGAGGGGGCAGGTGGTCCAGCTC

181' CTACAGGCCCCCTCAGATCGGCCTGATGTAACATTCAATGTGACTGGTGGTGAGTGGT
** ** **
181" CTGCAGGCCCCCACGGACCAGCGCGGGGTGACATTTAACCTGA---GCGGCGGCA-----

241' GGTGGCGGTGAGGCTGCTGGGGGGAACCTTCTGCTGTCAATATGGTGTGATGGGTGAGCAC
** *
233" ---GCAGCAAGGCTCCAGGGGGACCCTTCCACTGCCAGTATGGAGTGTTAGGTGAGCTC

301' AGTCAGCCCCAGCTGTGCGACTTCAGCCAGCAGGTGCAGGTCTCCTTCCCAGTCCCCACC
* **
289" AACCAGTCCCAGCTGTCAGACCTCAGCGAGCCCGTGAACGTCTCCTTCCCAGTGCCCACT

361' TGGATCTTGGCACTCTCCCTGAGCCTGGCTGGAG--CT-GTGCTGTTCTCAGGGCTGGTG
*****
349" TGGATCTTGGTGCTCTCCCTGAGCCTGGCTGGTGCCCTCTTCTCCTTGCTGGGCTGGTG

418' GCCATCACAGTGCTGGTGAGAAAAGCTAAAGCCAAAAAATTACAGAAGCAGAGAGAGCGT
** *
409" GCTGTTGCCCTGGTGGTCAGAAAAGTTAAACTCAGAAATTTACAGAAGAAAAGAGATCGA

478' GAATCCTGCTGGGCTCAGATCAACTTCACCAATACAGACATGTCCTTTGATAACTCTCTG
*****
469" GAATCCTGCTGGGCCAGATTAACCTTCGACAGCACAGACATGTCCTTCGATAACTCCCTG

538' TTTGCTATCTCCACGAAAA---TGACTCAGGAAGA-----
*** *
529" TTTACCGTCTCCGCGAAAAACGATGCCAGAAGAAGACCGGCCACCTTGGATGATCACTCA

570' ---CTCAGTGGCAACCCTAG--ACTCAGGGCCTCGGAAGAGGCCACCTCTGCATCATCC
** **
589" GGCACCACTGCCACCCCAGCAACTCCAGGACCCGGAAGAGGCCCACTTCCACGTCCTCC

625' TCTCCGGAGCCCCCTGAGTTCAGCACTTTCCGGGCCTGCCAG (SEQ ID NO :1)
** **
649' TCGCCTGAGACCCCGAATTACAGCACTTTCCGGGCCTGCCAG (SEQ ID NO :5)

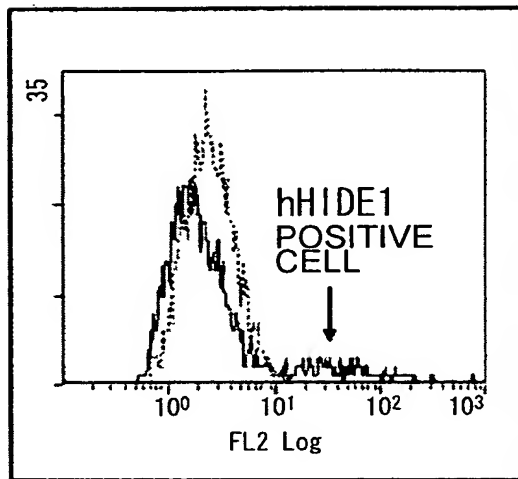
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FIG. 3

SEQUENCE 1	:	MOUSE	HIDE1 (mHIDE1)
AMINO ACID LENGTH	:	222	
MATCHING POSITION	:	1 - 222	
SEQUENCE 2	:	HUMAN	HIDE1 (hHIDE1)
AMINO ACID LENGTH	:	230	
MATCHING POSITION	:	1 - 230	
SEQUENCE HOMOMOLOGY	:	68.38 [%]	
mHIDE1 : 1	:	MPWTILLFAS GSLAIPAPSI SLVPPYPSSH EDPIVISCTA PGDILGANFT LFRGGEVVQL	
	:	*****	*****
hHIDE1 : 1	:	MPWTILLFAA GSLAIPAPSI RLVPYPSSQ EDPIHIACMA PGNFPGANFT LYRGQVVQL	
61 :	:	LQAPSDRPDV TFNVTGGSG GGGEAAGGNF CCQYGVMEH SQQLSDFSQ QVQVSFPVPT	
	:	**** *	**** *
61 :	:	LQAPTDQRGV TFN----LSG GSSKAPGGPF HCQYGVLGEL NQQLSDLSE PVNVSFPVPT	
121 :	:	WILALSLSLA GA-VLFSLV AITVLVRKAK AKNLQKQER ESCWAQINFT NTDMSFDNSL	
	:	*** *****	*** *****
117 :	:	WILVLSLSLA GALFLLAGLV AVALVVRKVK LRNLQKXDR ESCWAQINFD STDMSFDNSL	
180 :	:	FAISTKMTQE DSVATLD--- -----SG PRKRPTSASS SPEPPEFSTF RACQ(seq ID NO:2)	
	:	* * *	* * *
177 :	:	FTVSAKTMPE EDPATLDDHS GTTATPSNSR TRKRPTSTSS SPETPEFSTF RACQ(seq ID NO:6)	
	:	* * *	* * *

FIG. 4

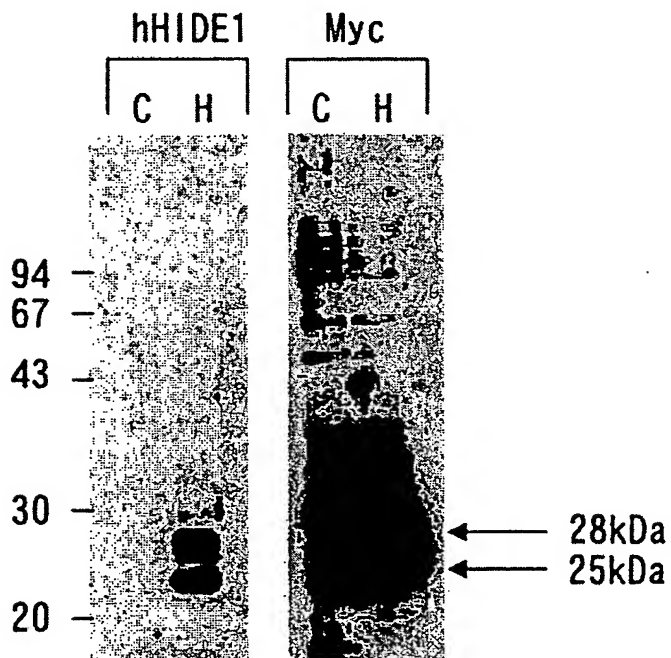
a



PE

b

W. B.



c

I. P.

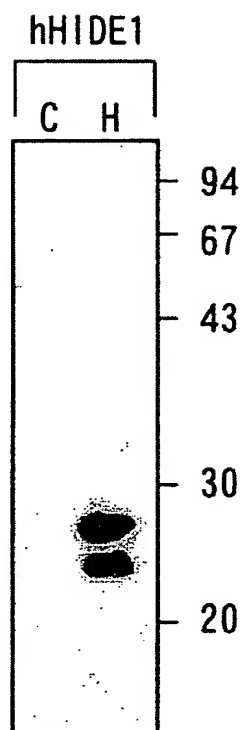
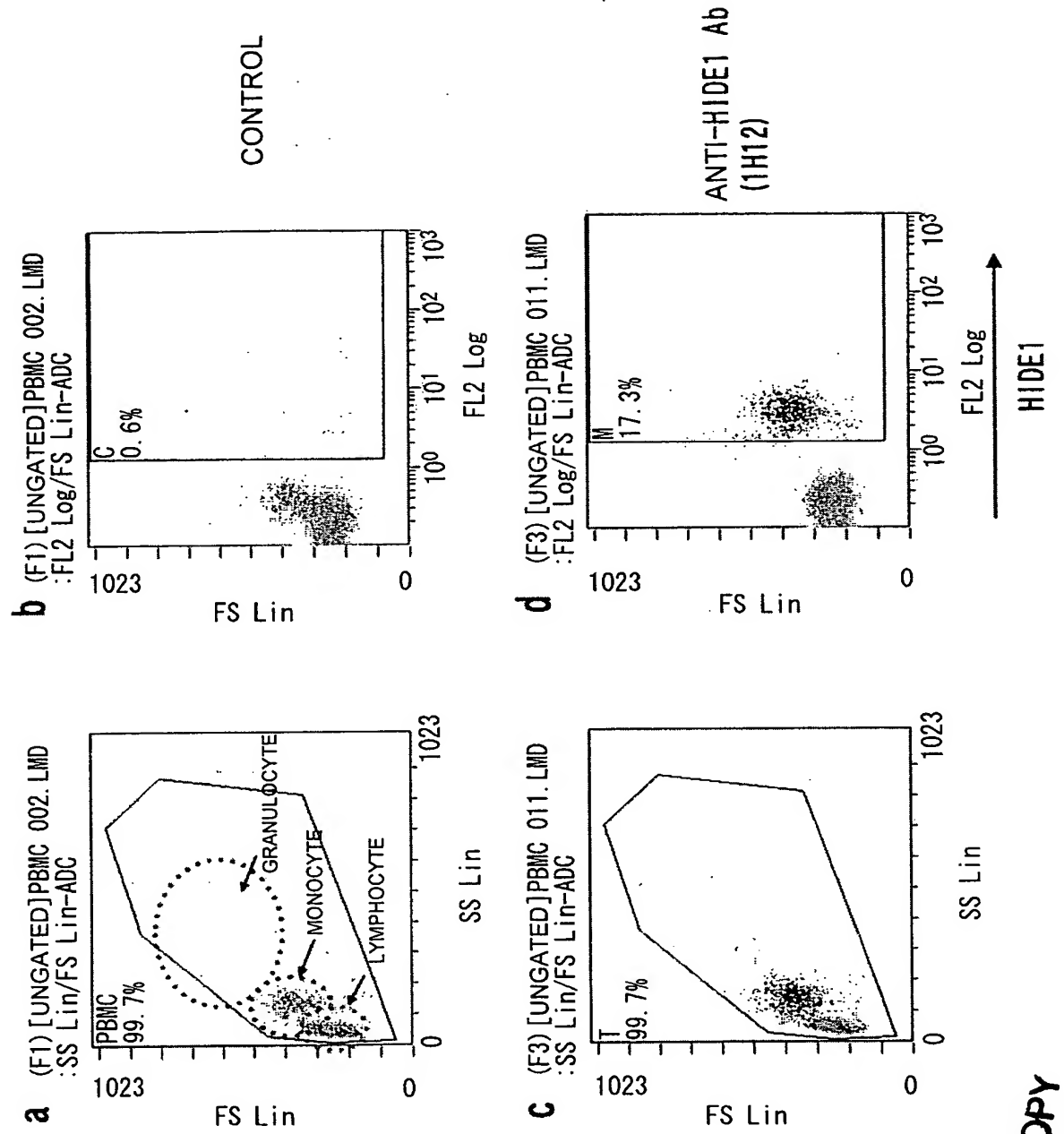
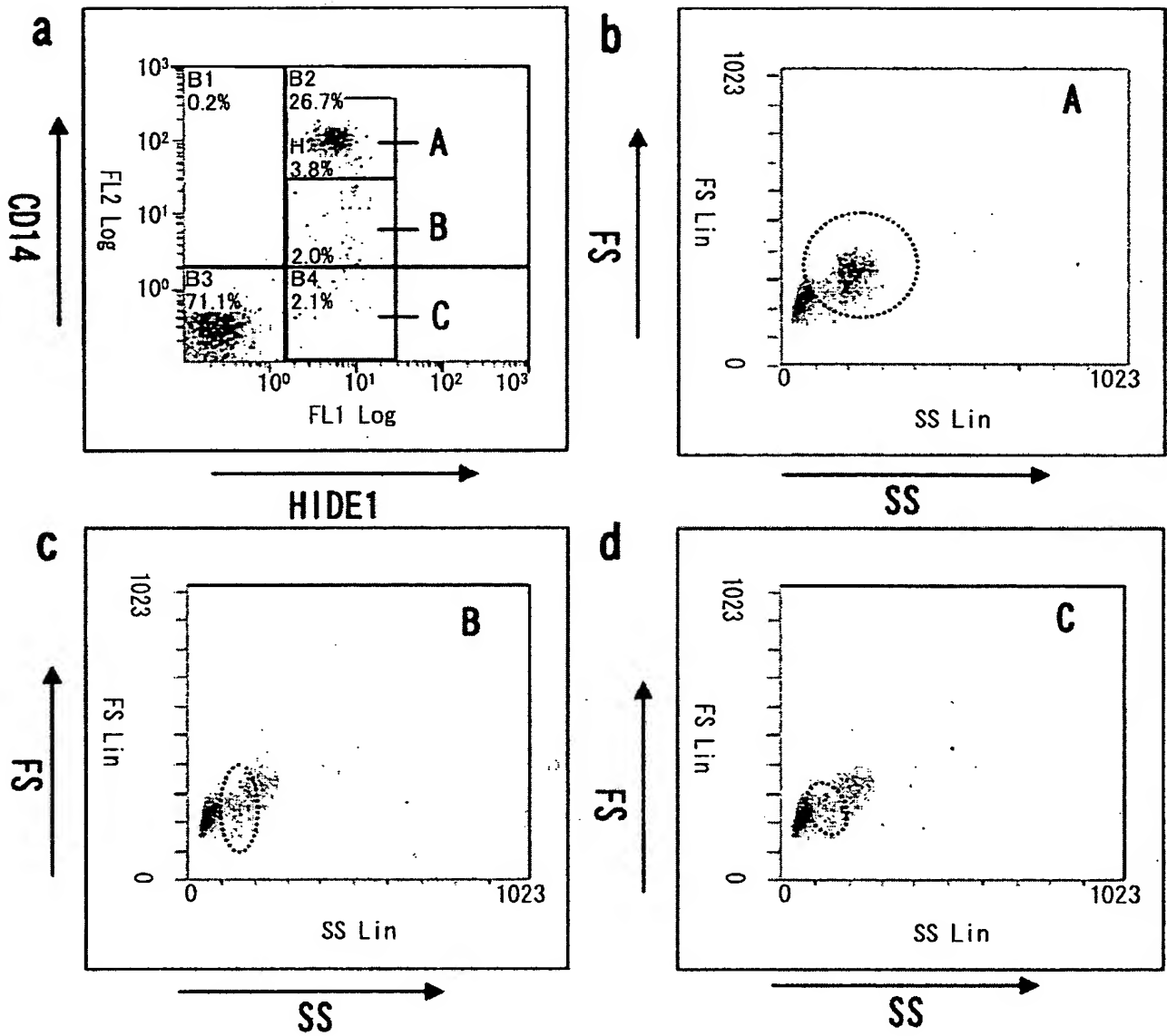


FIG. 5



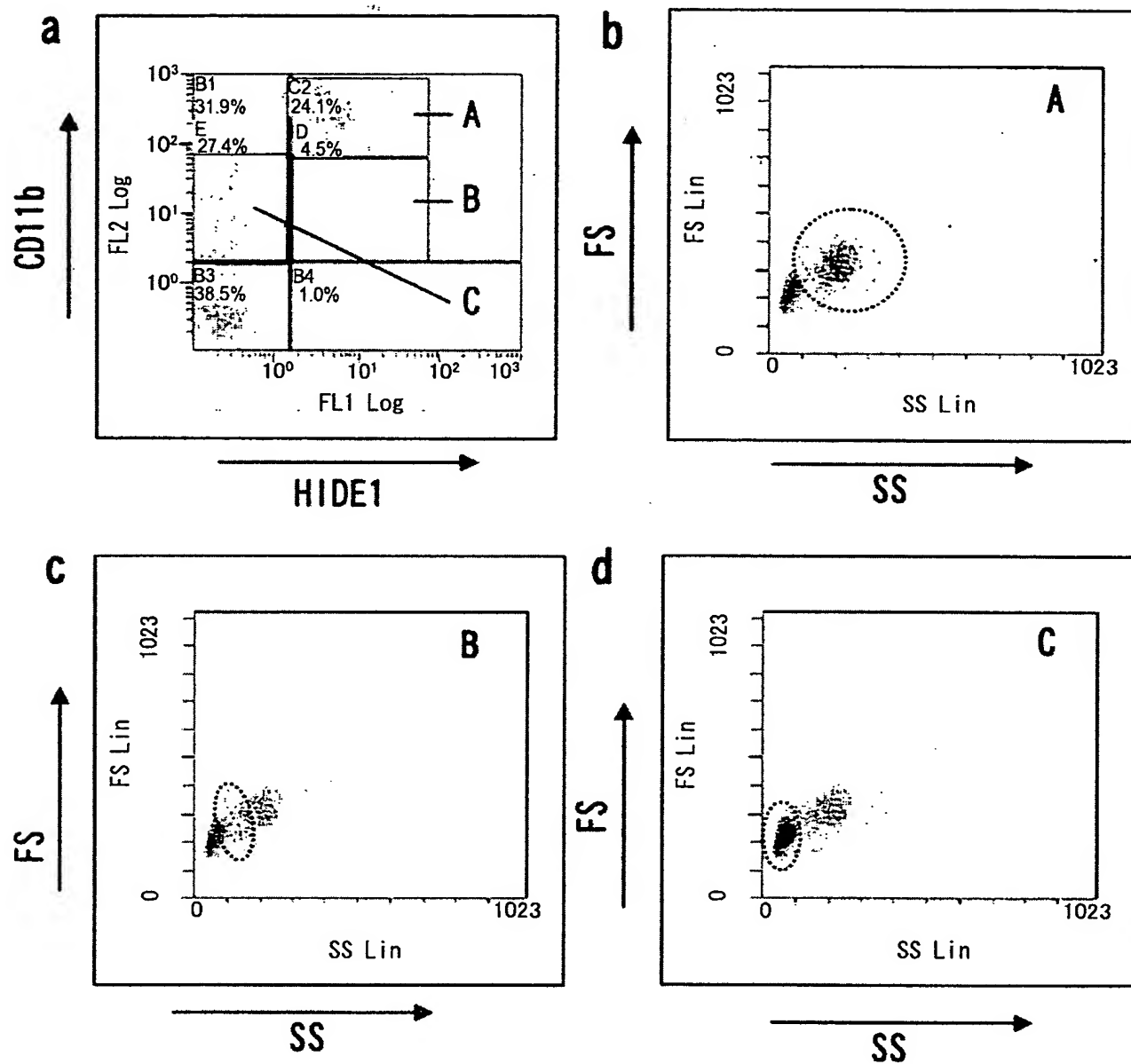
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FIG. 6



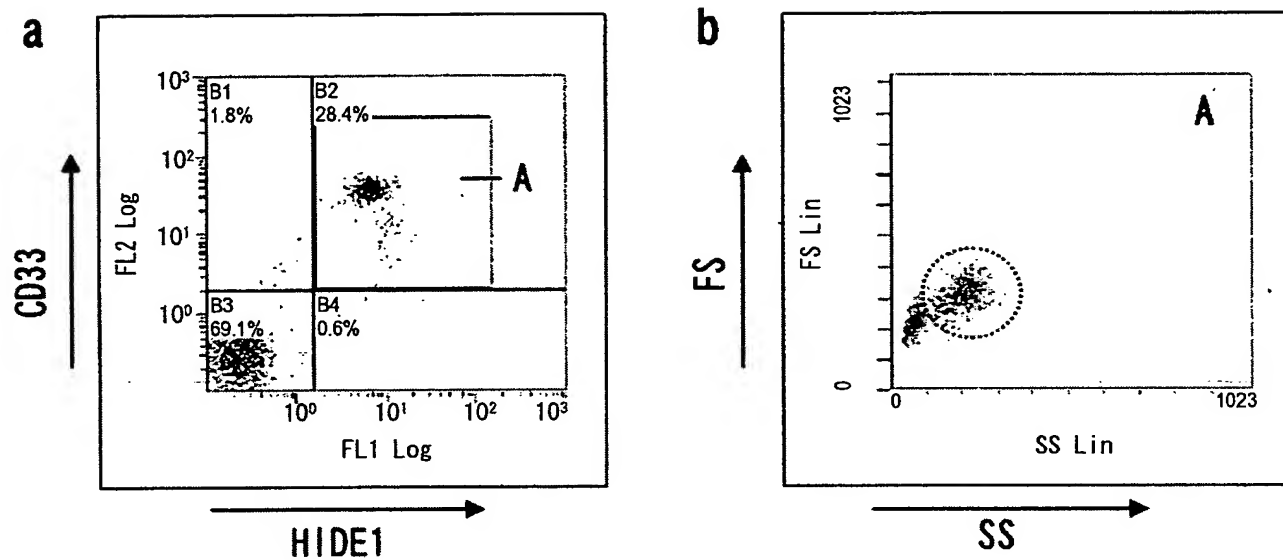
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FIG. 7



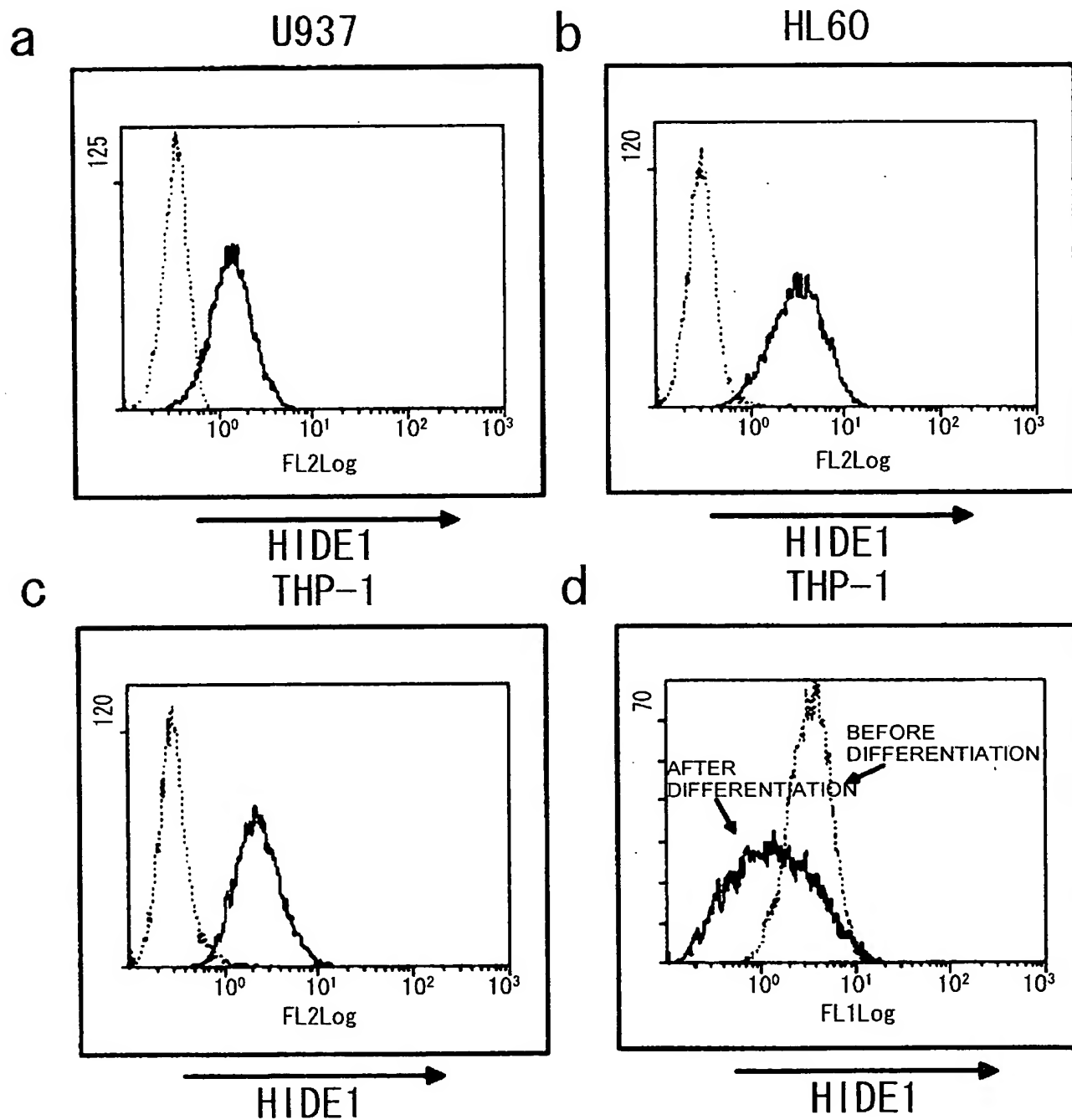
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FIG. 8



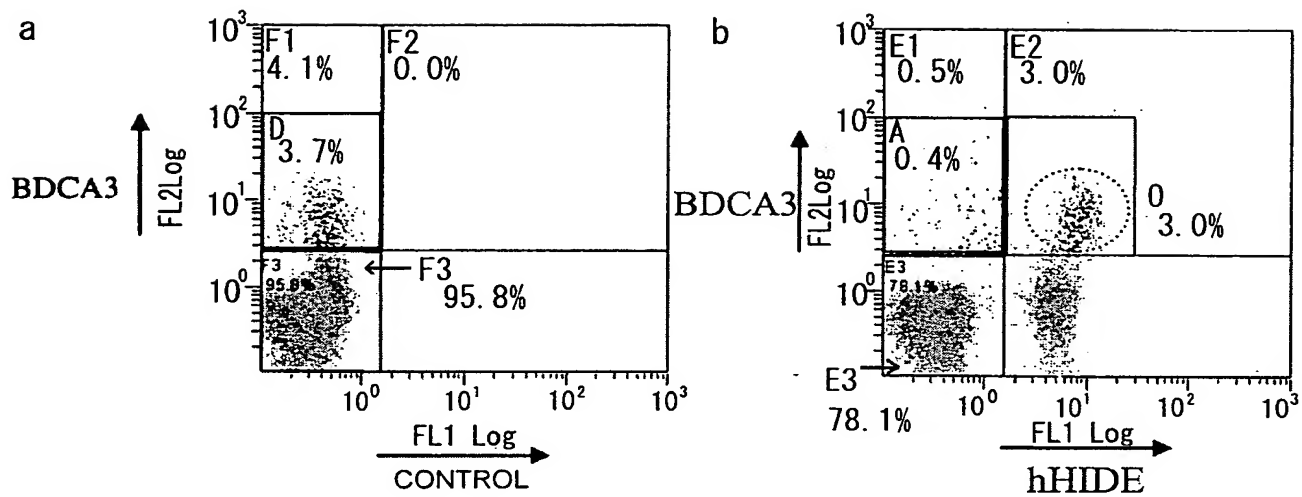
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FIG. 9



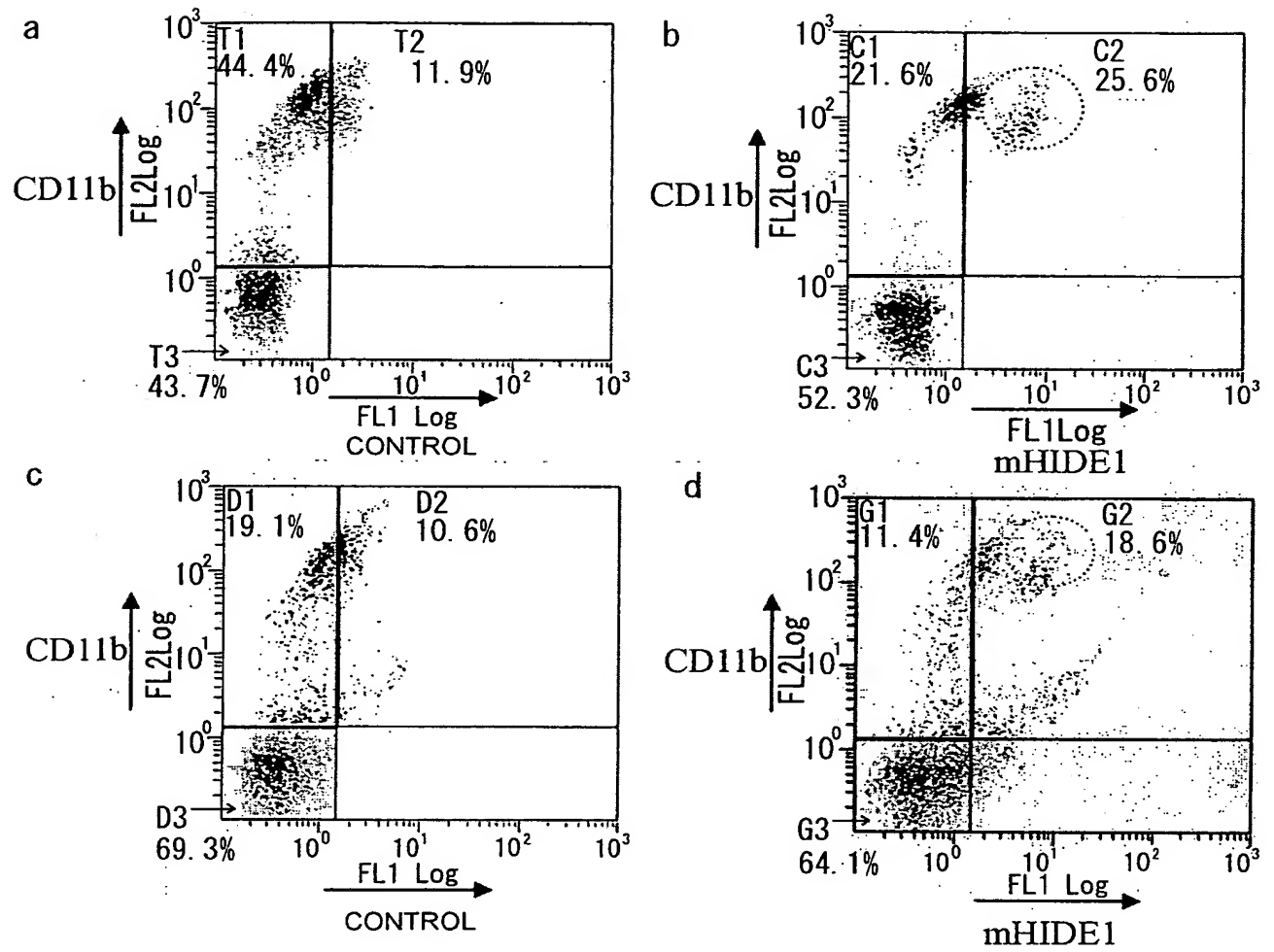
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FIG. 10



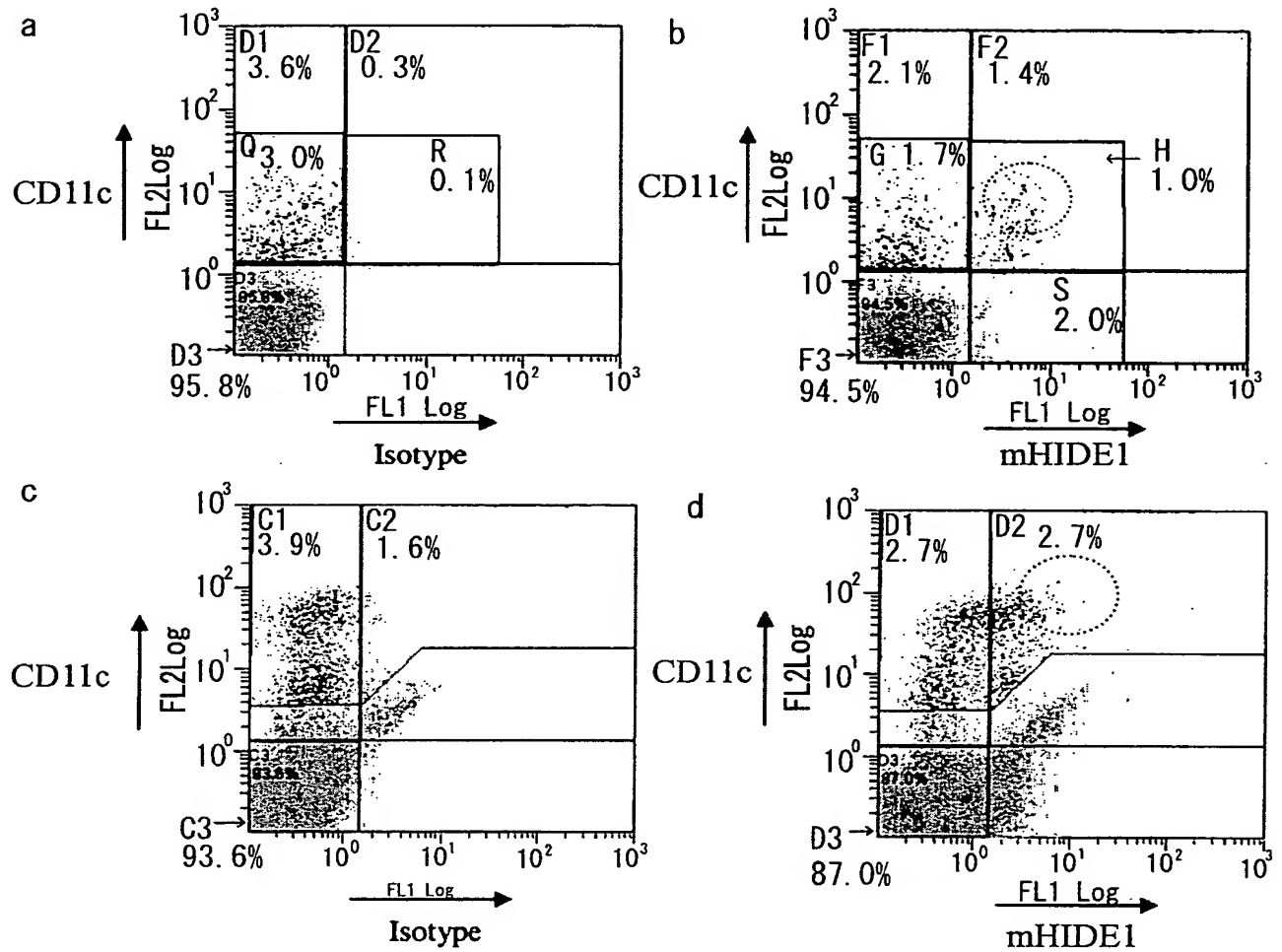
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FIG. 11



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FIG. 12



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